<110> Walker, David H.
McBride, Jere W.
Yu, Xue-Jie

<120> Homologous 28-Kilodalton Immunodominant Protein Genes of *Ehrlichia canis* and Uses Thereof

<130> D6152CIP2/D1

<141> 2002-01-31

<150> 09/660,587
<151> 2000-09-12

<160> 46

<210> 1
<211> 1607
<212> DNA
<213> *Ehrlichia canis*

<220>
<223> nucleic acid sequence of *E. canis p28-7*

<400> 1

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gcacttccac tattgttaat ttatttcac tattttaggt gtaatatgaa 150
ttgcaaaaaa attcttataa caactgcatt aatatcatta atgtactcta 200
ttccaagcat atctttttct gatactatac aagatggtaa catgggtggt 250
aacttctata ttagtggaaa gtatgtacca agtgtctcac attttggtag 300
cttctcagct aaagaagaaa gcaaatcaac tgttggagtt tttggattaa 350
aacatgattg ggatggaagt ccaatactta agaataaaca cgctgacttt 400
actgttccaa actattcgtt cagatacgag aacaatccat ttctagggtt 450
tgcaggagct atcggttact caatgggtgg cccaagaata gaattcgaaa 500
tatcttatga agcattcgac gtaaaaagtc ctaatatcaa ttatcaaaat 550
gacgcgcaca ggtactgcgc tctatctcat cacacatcgg cagccatgga 600
agctgataaa tttgtcttct taaaaaacga agggttaatt gacatatcac 650

ttgcaataaa tgcatgttat gatataataa atgacaaagt acctgtttct 700
ccttatatat gcgcaggtat tggtactgat ttgatttcta tgtttgaagc 750
tacaagtcct aaaatttcct accaaggaaa actgggcatt agttactcta 800
ttaatccgga aacctctgtt ttcatcggtg ggcatttcca caggatcata 850
ggtaatgagt ttagagatat tcctgcaata gtacctagta actcaactac 900
aataagtgga ccacaatttg caacagtaac actaaatgtg tgtcactttg 950
gtttagaact tggaggaaga tttaacttct aattttattg ttgccacata 1000
ttaaaaatga tctaaacttg tttttawtat tgctacatac aaaaaaagaa 1050
aaatagtggc aaaagaatgt agcaataaga ggggggggggg ggaccaaatt 1100
tatcttctat gcttcccaag ttttttcycg ctatttatga cttaaacaac 1150
agaaggtaat atcctcacgg aaaacttatc ttcaaatatt ttatttatta 1200
ccaatcttat ataatatatt aaatttctct tacaaaaatc actagtattt 1250
tataccaaaa tatatattct gacttgcttt tcttctgcac ttctactatt 1300
tttaatttat ttgtcactat taggttataa taawatgaat tgcmaaagat 1350
ttttcatagc aagtgcattg atatcactaa tgtctttctt acctagcgta 1400
tctttttctg aatcaataca tgaagataat ataaatggta acttttacat 1450
tagtgcaaag tatatgccaa gtgcctcaca ctttggcgta ttttcagtta 1500
aagaagagaa aaacacaaca actggagttt tcggattaaa acaagattgg 1550
gacggagcaa cactaaagga tgcaagcwgc agccacacaw tagacccaag 1600
tacaatg 1607

<210> 2
<211> 278
<212> PRT
<213> *Ehrlichia canis*

<220>
<223> amino acid sequence of *E. canis* p28-7 protein

<400> 2

Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Ile Ser Leu
5 10 15
Met Tyr Ser Ile Pro Ser Ile Ser Phe Ser Asp Thr Ile Gln Asp
20 25 30

Gly Asn Met Gly Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Val Pro
35 40 45
Ser Val Ser His Phe Gly Ser Phe Ser Ala Lys Glu Glu Ser Lys
50 55 60
Ser Thr Val Gly Val Phe Gly Leu Lys His Asp trp Asp Gly Ser
65 70 75
Pro Ile Leu Lys Asn Lys His Ala Asp Phe Thr Val Pro Asn Tyr
80 85 90
Ser Phe Arg Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala
95 100 105
Ile Gly Tyr Ser Met Gly Gly Pro Arg Ile Glu Phe Glu Ile Ser
110 115 120
Tyr Glu Ala Phe Asp Val Lys Ser Pro Asn Ile Asn Tyr Gln Asn
125 130 135
Asp Ala His Arg Tyr Cys Ala Leu Ser His His Thr Ser Ala Ala
140 145 150
Met Glu Ala Asp Lys Phe Val Phe Leu Lys Asn Glu Gly Leu Ile
155 160 165
Asp Ile Ser Leu Ala Ile Asn Ala Cys Tyr Asp Ile Ile Asn Asp
170 175 180
Lys Val Pro Val Ser Pro Tyr Ile Cys Ala Gly Ile Gly Thr Asp
185 190 195
Leu Ile Ser Met Phe Glu Ala Thr Ser Pro Lys Ile Ser Tyr Gln
200 205 210
Gly Lys Leu Gly Ile Ser Tyr Ser Ile Asn Pro Glu Thr Ser Val
215 220 225
Phe Ile Gly Gly His Phe His Arg Ile Ile Gly Asn Glu Phe Arg
230 235 240
Asp Ile Pro Ala Ile Val Pro Ser Asn Ser Thr Thr Ile Ser Gly
245 250 255
Pro Gln Phe Ala Thr Val Thr Leu Asn Val Cys His Phe Gly Leu
260 265 270
Glu Leu Gly Gly Arg Phe Asn Phe
275

<210> 3
<211> 849
<212> DNA
<213> *Ehrlichia canis*

<220>
<221> mat_peptide
<223> nucleic acid sequence of *p28-5*

<400> 3

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atggtaattt ttacatatca ggaaagtaca tgccaagtgt tcctcatttt 150
ggaatttttt cagctgaaga agagaaaaaa aagacaactg tagtatatgg 200
cttaaaagaa aactgggcag gagatgcaat atctagtcaa agtccagatg 250
ataattttac cattcgaaat tactcattca agtatgcaag caacaagttt 300
ttagggtttg cagtagctat tggttactcg ataggcagtc caagaataga 350
agttgagatg tcttatgaag catttgatgt gaaaaatcca ggtgataatt 400
acaaaaacgg tgcttacagg tattgtgctt tatctcatca agatgatgcg 450
gatgatgaca tgactagtgc aactgacaaa tttgtatatt taattaatga 500
aggattactt aacatatcat ttatgacaaa catatgttat gaaacagcaa 550
gcaaaaatat acctctctct ccttacatat gtgcaggtat tggtactgat 600
ttaattcaca tgtttgaaac tacacatcct aaaatttctt atcaaggaaa 650
gctagggttg gcctacttcg taagtgcaga gtcttcggtt tcttttggta 700
tatattttca taaaattata aataataagt ttaaaaatgt tccagccatg 750
gtacctatta actcagacga gatagtagga ccacagtttg caacagtaac 800
attaaatgta tgctactttg gattagaact tggatgtagg ttcaacttc 849

<210> 4
<211> 283
<212> PRT
<213> *Ehrlichia canis*

<220>
<223> amino acid sequence of p28-5 protein

<400> 4

Met Asn Cys Lys Lys Val Phe Thr Ile Ser Ala Leu Ile Ser Ser
5 10 15
Ile Tyr Phe Leu Pro Asn Val Ser Tyr Ser Asn Pro Val Tyr Gly
20 25 30
Asn Ser Met Tyr Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro
35 40 45
Ser Val Pro His Phe Gly Ile Phe Ser Ala Glu Glu Glu Lys Lys
50 55 60
Lys Thr Thr Val Val Tyr Gly Leu Lys Glu Asn Trp Ala Gly Asp
65 70 75
Ala Ile Ser Ser Gln Ser Pro Asp Asp Asn Phe Thr Ile Arg Asn
80 85 90
Tyr Ser Phe Lys Tyr Ala Ser Asn Lys Phe Leu Gly Phe Ala Val
95 100 105
Ala Ile Gly Tyr Ser Ile Gly Ser Pro Arg Ile Glu Val Glu Met
110 115 120
Ser Tyr Glu Ala Phe Asp Val Lys Asn Pro Gly Asp Asn Tyr Lys
125 130 135
Asn Gly Ala Tyr Arg Tyr Cys Ala Leu Ser His Gln Asp Asp Ala
140 145 150
Asp Asp Asp Met Thr Ser Ala Thr Asp Lys Phe Val Tyr Leu Ile
155 160 165
Asn Glu Gly Leu Leu Asn Ile Ser Phe Met Thr Asn Ile Cys Tyr
170 175 180
Glu Thr Ala Ser Lys Asn Ile Pro Leu Ser Pro Tyr Ile Cys Ala
185 190 195
Gly Ile Gly Thr Asp Leu Ile His Met Phe Glu Thr Thr His Pro
200 205 210
Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ala Tyr Phe Val Ser
215 220 225
Ala Glu Ser Ser Val Ser Phe Gly Ile Tyr Phe His Lys Ile Ile
230 235 240
Asn Asn Lys Phe Lys Asn Val Pro Ala Met Val Pro Ile Asn Ser
245 250 255

Asp Glu Ile Val Gly Pro Gln Phe Ala Thr Val Thr Leu Asn Val
260 265 270
Cys Tyr Phe Gly Leu Glu Leu Gly Cys Arg Phe Asn Phe
275 280

<210> 5
<211> 840
<212> DNA
<213> *Ehrlichia canis*

<220>
<221> mat_peptide
<223> nucleic acid sequence of *p28-6*

<400> 5
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ctatgctcca agcatatctt tttctgatac tatacaagac gataacactg 100
gtagcttcta catcagtgga aaatatgtac caagtgtttc acattttggt 150
gttttctcag ctaaagaaga aagaaactca actgttggag tttttggatt 200
aaaacatgat tggaatggag gtacaatatc taactcttct ccagaaaata 250
tattcacagt tcaaaattat tcgtttaaat acgaaaacaa cccattctta 300
gggtttgcag gagctattgg ttattcaatg ggtggcccaa gaatagaact 350
tgaagttctg tacgagacat tcgatgtgaa aaatcagaac aataattata 400
agaacggcgc acacagatac tgtgctttat ctcatcatag ttcagcaaca 450
agcatgtcct ccgcaagtaa caaatttgtt ttcttaaaaa atgaagggtt 500
aattgactta tcatttatga taaatgcatg ctatgacata ataattgaag 550
gaatgccttt ttcaccttat atttgtgcag gtgttggtac tgatgttgtt 600
tccatgtttg aagctataaa tcctaaaatt tcttaccaag gaaaactagg 650
attaggttat agtataagtt cagaagcctc tgtttttatc ggtggacact 700
ttcacagagt cataggtaat gaatttagag acatccctgc tatggttcct 750
agtggatcaa atcttccaga aaaccaattt gcaatagtaa cactaaatgt 800
gtgtcacttt ggcatagaac ttggaggaag atttaacttc 840

<210> 6
<211> 280
<212> PRT
<213> *Ehrlichia canis*

<220>
<223> amino acid sequence of p28-6 protein

<400> 6

Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Met Ser Leu
5 10 15
Met Tyr Tyr Ala Pro Ser Ile Ser Phe Ser Asp Thr Ile Gln Asp
20 25 30
Asp Asn Thr Gly Ser Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser
35 40 45
Val Ser His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Ser
50 55 60
Thr Val Gly Val Phe Gly Leu Lys His Asp Trp Asn Gly Gly Thr
65 70 75
Ile Ser Asn Ser Ser Pro Glu Asn Ile Phe Thr Val Gln Asn Tyr
80 85 90
Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala
95 100 105
Ile Gly Tyr Ser Met Gly Gly Pro Arg Ile Glu Leu Glu Val Leu
110 115 120
Tyr Glu Thr Phe Asp Val Lys Asn Gln Asn Asn Asn Tyr Lys Asn
125 130 135
Gly Ala His Arg Tyr Cys Ala Leu Ser His His Ser Ser Ala Thr
140 145 150
Ser Met Ser Ser Ala Ser Asn Lys Phe Val Phe Leu Lys Asn Glu
155 160 165
Gly Leu Ile Asp Leu Ser Phe Met Ile Asn Ala Cys Tyr Asp Ile
170 175 180
Ile Ile Glu Gly Met Pro Phe Ser Pro Tyr Ile Cys Ala Gly Val
185 190 195

Gly Thr Asp Val Val Ser Met Phe Glu Ala Ile Asn Pro Lys Ile
200 205 210
Ser Tyr Gln Gly Lys Leu Gly Leu Gly Tyr Ser Ile Ser Ser Glu
215 220 225
Ala Ser Val Phe Ile Gly Gly His Phe His Arg Val Ile Gly Asn
230 235 240
Glu Phe Arg Asp Ile Pro Ala Met Val Pro Ser Gly Ser Asn Leu
245 250 255
Pro Glu Asn Gln Phe Ala Ile Val Thr Leu Asn Val Cys His Phe
260 265 270
Gly Ile Glu Leu Gly Gly Arg Phe Asn Phe
275 280

<210> 7
<211> 133
<212> PRT
<213> *Ehrlichia canis*

<220>
<223> partial amino acid sequence of p28-5 protein

<400> 7

Met Asn Cys Lys Lys Val Phe Thr Ile Ser Ala Leu Ile Ser Ser
5 10 15
Ile Tyr Phe Leu Pro Asn Val Ser Tyr Ser Asn Pro Val Tyr Gly
20 25 30
Asn Ser Met Tyr Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro
35 40 45
Ser Val Pro His Phe Gly Ile Phe Ser Ala Glu Glu Glu Lys Lys
50 55 60
Lys Thr Thr Val Val Tyr Gly Leu Lys Glu Asn Trp Ala Gly Asp
65 70 75
Ala Ile Ser Ser Gln Ser Pro Asp Asp Asn Phe Thr Ile Arg Asn
80 85 90

Tyr Ser Phe Lys Tyr Ala Ser Asn Lys Phe Leu Gly Phe Ala Val
95 100 105
Ala Ile Gly Tyr Ser Ile Gly Ser Pro Arg Ile Glu Val Glu Met
110 115 120
Ser Tyr Glu Ala Phe Asp Val Lys Asn Gln Gly Asn Asn
125 130

<210> 8
<211> 287
<212> PRT
<213> *Ehrlichia canis*

<220>
<223> amino acid sequence of p28-4 protien

<400> 8

Met Lys Tyr Lys Lys Thr Phe Thr Val Thr Ala Leu Val Leu Leu
5 10 15
Thr Ser Phe Thr His Phe Ile Pro Phe Tyr Ser Pro Ala Arg Ala
20 25 30
Ser Thr Ile His Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Thr
35 40 45
Ala Ser His Phe Gly Ile Phe Ser Ala Lys Glu Glu Gln Ser Phe
50 55 60
Thr Lys Val Leu Val Gly Leu Asp Gln Arg Leu Ser His Asn Ile
65 70 75
Ile Asn Asn Asn Asp Thr Ala Lys Ser Leu Lys Val Gln Asn Tyr
80 85 90
Ser Phe Lys Tyr Lys Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala
95 100 105
Ile Gly Tyr Ser Ile Gly Asn Ser Arg Ile Glu Leu Glu Val Ser
110 115 120
His Glu Ile Phe Asp Thr Lys Asn Pro Gly Asn Asn Tyr Leu Asn
125 130 135

Asp Ser His Lys Tyr Cys Ala Leu Ser His Gly Ser His Ile Cys
140 145 150
Ser Asp Gly Asn Ser Gly Asp Trp Tyr Thr Ala Lys Thr Asp Lys
155 160 165
Phe Val Leu Leu Lys Asn Glu Gly Leu Leu Asp Val Ser Phe Met
170 175 180
Leu Asn Ala Cys Tyr Asp Ile Thr Thr Glu Lys Met Pro Phe Ser
185 190 195
Pro Tyr Ile Cys Ala Gly Ile Gly Thr Asp Leu Ile Ser Met Phe
200 205 210
Glu Thr Thr Gln Asn Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu
215 220 225
Asn Tyr Thr Ile Asn Ser Arg Val Ser Val Phe Ala Gly Gly His
230 235 240
Phe His Lys Val Ile Gly Asn Glu Phe Lys Gly Ile Pro Thr Leu
245 250 255
Leu Pro Asp Gly Ser Asn Ile Lys Val Gln Gln Ser Ala Thr Val
260 265 270
Thr Leu Asp Val Cys His Phe Gly Leu Glu Ile Gly Ser Arg Phe
275 280 285
Phe Phe

<210> 9
<211> 281
<212> PRT
<213> *Ehrlichia chaffeensis*

<220>
<223> amino acid sequence of *E. chaffeensis* P28

<400> 9

Met Asn Tyr Lys Lys Val Phe Ile Thr Ser Ala Leu Ile Ser Leu
5 10 15

Ile Ser Ser Leu Pro Gly Val Ser Phe Ser Asp Pro Ala Gly Ser
20 25 30
Gly Ile Asn Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser
35 40 45
Ala Ser His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr
50 55 60
Thr Val Gly Val Phe Gly Leu Lys Gln Asn Trp Asp Gly Ser Ala
65 70 75
Ile Ser Asn Ser Ser Pro Asn Asp Val Phe Thr Val Ser Asn Tyr
80 85 90
Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala
95 100 105
Ile Gly Tyr Ser Met Asp Gly Pro Arg Ile Glu Leu Glu Val Ser
110 115 120
Tyr Glu Thr Phe Asp Val Lys Asn Gln Gly Asn Asn Tyr Lys Asn
125 130 135
Glu Ala His Arg Tyr Cys Ala Leu Ser His Asn Ser Ala Ala Asp
140 145 150
Met Ser Ser Ala Ser Asn Asn Phe Val Phe Leu Lys Asn Glu Gly
155 160 165
Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr Asp Val Val
170 175 180
Gly Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala Gly Ile Gly
185 190 195
Thr Asp Leu Val Ser Met Phe Glu Ala Thr Asn Pro Lys Ile Ser
200 205 210
Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro Glu Ala
215 220 225
Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu
230 235 240
Phe Arg Asp Ile Pro Thr Ile Ile Pro Thr Gly Ser Thr Leu Ala
245 250 255
Gly Lys Gly Asn Tyr Pro Ala Ile Val Ile Leu Asp Val Cys His
260 265 270

Phe Gly Ile Glu Leu Gly Gly Arg Phe Ala Phe
275 280

<210> 10
<211> 283
<212> PRT
<213> *Ehrlichia chaffeensis*

<220>
<223> amino acid sequence of *E. chaffeensis* OMP-1B

<400> 10
Met Asn Tyr Lys Lys Ile Phe Val Ser Ser Ala Leu Ile Ser Leu
5 10 15
Met Ser Ile Leu Pro Tyr Gln Ser Phe Ala Asp Pro Val Thr Ser
20 25 30
Asn Asp Thr Gly Ile Asn Asp Ser Arg Glu Gly Phe Tyr Ile Ser
35 40 45
Val Lys Tyr Asn Pro Ser Ile Ser His Phe Arg Lys Phe Ser Ala
50 55 60
Glu Glu Ala Pro Ile Asn Gly Asn Thr Ser Ile Thr Lys Lys Val
65 70 75
Phe Gly Leu Lys Lys Asp Gly Asp Ile Ala Gln Ser Ala Asn Phe
80 85 90
Asn Arg Thr Asp Pro Ala Leu Glu Phe Gln Asn Asn Leu Ile Ser
95 100 105
Gly Phe Ser Gly Ser Ile Gly Tyr Ala Met Asp Gly Pro Arg Ile
110 115 120
Glu Leu Glu Ala Ala Tyr Gln Lys Phe Asp Ala Lys Asn Pro Asp
125 130 135
Asn Asn Asp Thr Asn Ser Gly Asp Tyr Tyr Lys Tyr Phe Gly Leu
140 145 150
Ser Arg Glu Asp Ala Ile Ala Asp Lys Lys Tyr Val Val Leu Lys
155 160 165

Asn Glu Gly Ile Thr Phe Met Ser Leu Met Val Asn Thr Cys Tyr
170 175 180
Asp Ile Thr Ala Glu Gly Val Pro Phe Ile Pro Tyr Ala Cys Ala
185 190 195
Gly Val Gly Ala Asp Leu Ile Asn Val Phe Lys Asp Phe Asn Leu
200 205 210
Lys Phe Ser Tyr Gln Gly Lys Ile Gly Ile Ser Tyr Pro Ile Thr
215 220 225
Pro Glu Val Ser Ala Phe Ile Gly Gly Tyr Tyr His Gly Val Ile
230 235 240
Gly Asn Asn Phe Asn Lys Ile Pro Val Ile Thr Pro Val Val Leu
245 250 255
Glu Gly Ala Pro Gln Thr Thr Ser Ala Leu Val Thr Ile Asp Thr
260 265 270
Gly Tyr Phe Gly Gly Glu Val Gly Val Arg Phe Thr Phe
275 280

<210> 11
<211> 280
<212> PRT
<213> *Ehrlichia chaffeensis*

<220>
<223> amino acid sequence of *E. chaffeensis* OMP-1C

<400> 11
Met Asn Cys Lys Lys Phe Phe Ile Thr Thr Ala Leu Ala Leu Pro
5 10 15
Met Ser Phe Leu Pro Gly Ile Leu Leu Ser Glu Pro Val Gln Asp
20 25 30
Asp Ser Val Ser Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro
35 40 45
Ser Ala Ser His Phe Gly Val Phe Ser Ala Lys Glu Glu Lys Asn
50 55 60

Pro Thr Val Ala Leu Tyr Gly Leu Lys Gln Asp Trp Asn Gly Val
65 70 75
Ser Ala Ser Ser His Ala Asp Ala Asp Phe Asn Asn Lys Gly Tyr
80 85 90
Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala
95 100 105
Ile Gly Tyr Ser Met Gly Gly Pro Arg Ile Glu Phe Glu Val Ser
110 115 120
Tyr Glu Thr Phe Asp Val Lys Asn Gln Gly Gly Asn Tyr Lys Asn
125 130 135
Asp Ala His Arg Tyr Cys Ala Leu Asp Arg Lys Ala Ser Ser Thr
140 145 150
Asn Ala Thr Ala Ser His Tyr Val Leu Leu Lys Asn Glu Gly Leu
155 160 165
Leu Asp Ile Ser Leu Met Leu Asn Ala Cys Tyr Asp Val Val Ser
170 175 180
Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala Gly Val Gly Thr
185 190 195
Asp Leu Ile Ser Met Phe Glu Ala Ile Asn Pro Lys Ile Ser Tyr
200 205 210
Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala Ser
215 220 225
Val Phe Val Gly Gly His Phe His Lys Val Ala Gly Asn Glu Phe
230 235 240
Arg Asp Ile Ser Thr Leu Lys Ala Phe Ala Thr Pro Ser Ser Ala
245 250 255
Ala Thr Pro Asp Leu Ala Thr Val Thr Leu Ser Val Cys His Phe
260 265 270
Gly Val Glu Leu Gly Gly Arg Phe Asn Phe
275 280

<210> 12
<211> 286
<212> PRT

SEQ 14

<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of *E. chaffeensis* OMP-1D

<400> 12

Met Asn Cys Glu Lys Phe Phe Ile Thr Thr Ala Leu Thr Leu Leu
5 10 15
Met Ser Phe Leu Pro Gly Ile Ser Leu Ser Asp Pro Val Gln Asp
20 25 30
Asp Asn Ile Ser Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro
35 40 45
Ser Ala Ser His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn
50 55 60
Thr Thr Val Gly Val Phe Gly Ile Glu Gln Asp Trp Asp Arg Cys
65 70 75
Val Ile Ser Arg Thr Thr Leu Ser Asp Ile Phe Thr Val Pro Asn
80 85 90
Tyr Ser Phe Lys Tyr Glu Asn Asn Leu Phe Ser Gly Phe Ala Gly
95 100 105
Ala Ile Gly Tyr Ser Met Asp Gly Pro Arg Ile Glu Leu Glu Val
110 115 120
Ser Tyr Glu Ala Phe Asp Val Lys Asn Gln Gly Asn Asn Tyr Lys
125 130 135
Asn Glu Ala His Arg Tyr Tyr Ala Leu Ser His Leu Leu Gly Thr
140 145 150
Glu Thr Gln Ile Asp Gly Ala Gly Ser Ala Ser Val Phe Leu Ile
155 160 165
Asn Glu Gly Leu Leu Asp Lys Ser Phe Met Leu Asn Ala Cys Tyr
170 175 180
Asp Val Ile Ser Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala
185 190 195
Gly Ile Gly Ile Asp Leu Val Ser Met Phe Glu Ala Ile Asn Pro
200 205 210

Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Pro Ile Ser
215 220 225
Pro Glu Ala Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile
230 235 240
Gly Asn Glu Phe Arg Asp Ile Pro Thr Met Ile Pro Ser Glu Ser
245 250 255
Ala Leu Ala Gly Lys Gly Asn Tyr Pro Ala Ile Val Thr Leu Asp
260 265 270
Val Phe Tyr Phe Gly Ile Glu Leu Gly Gly Arg Phe Asn Phe Gln
275 280 285
Leu

<210> 13
<211> 278
<212> PRT
<213> *Ehrlichia chaffeensis*

<220>
<223> amino acid sequence of *E. chaffeensis* OMP-1E

<400> 13
Met Asn Cys Lys Lys Phe Phe Ile Thr Thr Ala Leu Val Ser Leu
5 10 15
Met Ser Phe Leu Pro Gly Ile Ser Phe Ser Asp Pro Val Gln Gly
20 25 30
Asp Asn Ile Ser Gly Asn Phe Tyr Val Ser Gly Lys Tyr Met Pro
35 40 45
Ser Ala Ser His Phe Gly Met Phe Ser Ala Lys Glu Glu Lys Asn
50 55 60
Pro Thr Val Ala Leu Tyr Gly Leu Lys Gln Asp Trp Glu Gly Ile
65 70 75
Ser Ser Ser Ser His Asn Asp Asn His Phe Asn Asn Lys Gly Tyr
80 85 90
Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala
95 100 105

Ile Gly Tyr Ser Met Gly Gly Pro Arg Val Glu Phe Glu Val Ser
110 115 120
Tyr Glu Thr Phe Asp Val Lys Asn Gln Gly Asn Asn Tyr Lys Asn
125 130 135
Asp Ala His Arg Tyr Cys Ala Leu Gly Gln Gln Asp Asn Ser Gly
140 145 150
Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu Lys Ser Glu Gly Leu
155 160 165
Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr Asp Ile Ile Asn
170 175 180
Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly Val Gly Thr
185 190 195
Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile Ser Tyr
200 205 210
Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala Ser
215 220 225
Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu Phe
230 235 240
Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr
245 250 255
Pro Asp Leu Ala Ile Val Thr Leu Ser Val Cys His Phe Gly Ile
260 265 270
Glu Leu Gly Gly Arg Phe Asn Phe
275

<210> 14
<211> 280
<212> PRT
<213> *Ehrlichia chaffeensis*

<220>
<223> amino acid sequence of *E. chaffeensis* OMP-1F

<400> 14

Met Asn Cys Lys Lys Phe Phe Ile Thr Thr Thr Leu Val Ser Leu
5 10 15

Met Ser Phe Leu Pro Gly Ile Ser Phe Ser Asp Ala Val Gln Asn
20 25 30

Asp Asn Val Gly Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Val Pro
35 40 45

Ser Val Ser His Phe Gly Val Phe Ser Ala Lys Gln Glu Arg Asn
50 55 60

Thr Thr Thr Gly Val Phe Gly Leu Lys Gln Asp Trp Asp Gly Ser
65 70 75

Thr Ile Ser Lys Asn Ser Pro Glu Asn Thr Phe Asn Val Pro Asn
80 85 90

Tyr Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly
95 100 105

Ala Val Gly Tyr Leu Met Asn Gly Pro Arg Ile Glu Leu Glu Met
110 115 120

Ser Tyr Glu Thr Phe Asp Val Lys Asn Gln Gly Asn Asn Tyr Lys
125 130 135

Asn Asp Ala His Lys Tyr Tyr Ala Leu Thr His Asn Ser Gly Gly
140 145 150

Lys Leu Ser Asn Ala Gly Asp Lys Phe Val Phe Leu Lys Asn Glu
155 160 165

Gly Leu Leu Asp Ile Ser Leu Met Leu Asn Ala Cys Tyr Asp Val
170 175 180

Ile Ser Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala Gly Val
185 190 195

Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Ile Asn Pro Lys Ile
200 205 210

Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro Glu
215 220 225

Ala Ser Val Phe Val Gly Gly His Phe His Lys Val Ile Gly Asn
230 235 240

Glu Phe Arg Asp Ile Pro Ala Met Ile Pro Ser Thr Ser Thr Leu
245 250 255

Thr Gly Asn His Phe Thr Ile Val Thr Leu Ser Val Cys His Phe
260 265 270
Gly Val Glu Leu Gly Gly Arg Phe Asn Phe
275 280

<210> 15
<211> 284
<212> PRT
<213> *Cowdria ruminantium*

<220>
<223> amino acid sequence of *C. ruminantium* MAP-1

<400> 15
Met Asn Cys Lys Lys Ile Phe Ile Thr Ser Thr Leu Ile Ser Leu
5 10 15
Val Ser Phe Leu Pro Gly Val Ser Phe Ser Asp Val Ile Gln Glu
20 25 30
Glu Asn Asn Pro Val Gly Ser Val Tyr Ile Ser Ala Lys Tyr Met
35 40 45
Pro Thr Ala Ser His Phe Gly Lys Met Ser Ile Lys Glu Asp Ser
50 55 60
Arg Asp Thr Lys Ala Val Phe Gly Leu Lys Lys Asp Trp Asp Gly
65 70 75
Val Lys Thr Pro Ser Gly Asn Thr Asn Ser Ile Phe Thr Glu Lys
80 85 90
Asp Tyr Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala
95 100 105
Gly Ala Val Gly Tyr Ser Met Asn Gly Pro Arg Ile Glu Phe Glu
110 115 120
Val Ser Tyr Glu Thr Phe Asp Val Arg Asn Pro Gly Gly Asn Tyr
125 130 135
Lys Asn Asp Ala His Met Tyr Cys Ala Leu Asp Thr Ala Ser Ser
140 145 150

Ser Thr Ala Gly Ala Thr Thr Ser Val Met Val Lys Asn Glu Asn
155 160 165
Leu Thr Asp Ile Ser Leu Met Leu Asn Ala Cys Tyr Asp Ile Met
170 175 180
Leu Asp Gly Met Pro Val Ser Pro Tyr Val Cys Ala Gly Ile Gly
185 190 195
Thr Asp Leu Val Ser Val Ile Asn Ala Thr Asn Pro Lys Leu Ser
200 205 210
Tyr Gln Gly Lys Leu Gly Ile Ser Tyr Ser Ile Asn Pro Glu Ala
215 220 225
Ser Ile Phe Ile Gly Gly His Phe His Arg Val Ile Gly Asn Glu
230 235 240
Phe Lys Asp Ile Ala Thr Ser Lys Val Phe Thr Ser Ser Gly Asn
245 250 255
Ala Ser Ser Ala Val Ser Pro Gly Phe Ala Ser Ala Ile Leu Asp
260 265 270
Val Cys His Phe Gly Ile Glu Ile Gly Gly Arg Phe Val Phe
275 280

<210> 16
<211> 20
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<222> nucleotides 313-332 of *C. ruminantium MAP-1*, also nucleotides 307-326 of *E. chaffeensis P28*
<223> forward primer 793 for PCR

<400> 16
gcaggagctg ttggttactc 20

<210> 17
<211> 21
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<222> nucleotides 823-843 of *C. ruminantium MAP-1*, also nucleotides 814-834 of *E. chaffeensis P28*
<223> reverse primer 1330 for PCR

<400> 17
ccttcctcca agttctatgc c 21

<210> 18
<211> 24
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<223> primer 46f, specific for *p28-5* gene

<400> 18
atatacttcc tacctaatgt ctca 24

<210> 19
<211> 20
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind

<223> primer used for sequencing 28-kDa protein genes in *E. canis*

<400> 19
agtgcagagt cttcggtttc 20

<210> 20
<211> 18
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<223> primer used for sequencing 28-kDa protein genes in *E. canis*

<400> 20
gttacttgcg gaggacat 18

<210> 21
<211> 24
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<222> nucleotides 687-710 of *E. canis p28-7*
<223> primer 394 for PCR

<400> 21
gcatttccac aggatcatag gtaa 24

<210> 22
<211> 24
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<222> nucleotides 710-687 of *E. canis p28-7*
<223> primer 394C for PCR

<400> 22
ttacctatga tcctgtggaa atgc 24

<210> 23
<211> 20
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<223> primer 793C which anneals to a region with *E. canis p28-7*, used to amplify the intergenic region between gene *p28-6* and *p28-7*

<400> 23
gagtaaccaa cagctcctgc 20

<210> 24
<211> 24
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind

<222>

<223> primer EC28OM-F complementary to noncoding regions adjacent to the open reading frame of *p28-7*

<400> 24

tctactttgc acttccacta ttgt 24

<210> 25

<211> 24

<212> DNA

<213> artificial sequence

<220>

<221> primer_bind

<222>

<223> primer EC28OM-R complementary to noncoding regions adjacent to the open reading frame of *p28-7*

<400> 25

attcttttgc cactattttt cttt 24

<210> 26

<211> 25

<212> DNA

<213> artificial sequence

<220>

<221> primer_bind

<223> primer *ECaSA3-2* corresponding to regions within *p28-6*, used to amplify the intergenic region NC3 between gene *p28-6* and *p28-7*

<400> 26

ctaggattag gttatagtat aagtt 25

<210> 27
<211> 23
<212> PRT
<213> *Ehrlichia canis*

<220>
<221> PEPTIDE
<223> a predicted N-terminal signal peptide of p28-7 and p28-6

<400> 27
Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Met Ser Leu
5 10 15
Met Tyr Tyr Ala Pro Ser Ile Ser
20

<210> 28
<211> 25
<212> PRT
<213> *Ehrlichia chaffeensis*

<220>
<223> amino acid sequence of N-terminal signal peptide of *E. chaffeensis* P28

<400> 28
Met Asn Tyr Lys Lys Ile Leu Ile Thr Ser Ala Leu Ile Ser Leu
5 10 15
Ile Ser Ser Leu Pro Gly Val Ser Phe Ser
20 25

<210> 29
<211> 26

<212> PRT
<213> *Ehrlichia canis*

<220>
<223> amino acid sequence of putative cleavage site of *p28-7*

<400> 29
Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Ile Ser Leu
5 10 15
Met Tyr Ser Ile Pro Ser Ile Ser Ser Phe Ser
20 25

<210> 30
<211> 299
<212> DNA
<213> *Ehrlichia canis*

<220>
<223> nucleic acid sequence of intergenic noncoding region 1 (28NC1)

<400> 30
taatacttct attgtacatg ttaaaaatag tactagtttg cttctgtggt 50
ttataaacgc aagagagaaa tagttagtaa taaattagaa agttaaatat 100
tagaaaagtc atatgttttt cattgtcatt gatactcaac taaaagtagt 150
ataaatgtta cttattaata attttacgta gtatattaaa tttcccttac 200
aaaagccact agtattttat actaaaagct atactttggc ttgtatttaa 250
tttgtatttt tactactgtt aatttacttt cactgtttct ggtgtaaat 299

<210> 31
<211> 345
<212> DNA
<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic noncoding region 2 (28NC2)

<400> 31

taatttcgtg gtacacatat cacgaagcta aaattgtttt tttatctctg 50
ctgtatacaa gagaaaaaat agtagtgaaa attacctaac aatatgacag 100
tacaagttta ccaagcttat tctcacaaaa cttcttgtgt cttttatctc 150
tttacaatga aatgtacact tagcttcact actgtagagt gtgtttatca 200
atgctttgtt tattaatact ctacataata tgttaaattt ttcttacaaa 250
actcactagt aatttatact agaatatata ttctgacttg tatttgcttt 300
atacttccac tattgttaat ttattttcac tattttaggt gtaat 345

<210> 32

<211> 345

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic noncoding region 3 (28NC3)

<400> 32

tgattttatt gttgccacat attaaaaatg atctaaactt gtttttatta 50
ttgctacata caaaaaaaag aaaaatagtg gcaaaagaat gtagcaataa 100
gaggggggggg ggggactaaa tttaccttct attcttctaa tattctttac 150
tatattcaaa tagcacaact caatgcttcc aggaaaatat gtttctaata 200
ttttatttat taccaatcct tatataatat attaaatttc tcttacaaaa 250
atctctaatg ttttatactt aatatatata ttctggcttg tatttacttt 300
gcacttccac tattgttaat ttattttcac tattttaggt gtaat 345

<210> 33

<211> 355

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic noncoding region 4 (28NC4)

<400> 33

taattttatt gttgccacat attaaaaatg atctaaactt gtttttawta 50
ttgctacata caaaaaaaga aaaatagtgg caaaagaatg tagcaataag 100
agggggggggg gggaccaaat ttatcttcta tgcttcccaa gttttttcyc 150
gctatttatg acttaaacaa cagaaggtaa tatcctcacg gaaaacttat 200
cttcaaatat tttatttatt accaatctta tataatatat taaatttctc 250
ttacaaaaat cactagtatt ttataccaaa atatatattc tgacttgctt 300
ttcttctgca cttctactat ttttaattta tttgtcacta ttaggttata 350
ataaw 355

<210> 34

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> primer p28-5-818f

<400> 34

ttaaacatat gccacttcgg acta 24

<210> 35

<211> 28

<212> DNA

<213> artificial sequence

<220>

<223> primer 1191

<400> 35
tatgatcgtg taaaattgct gtgagtat 28

<210> 36
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> primer ECa28-75C

<400> 36
tactggcacg tgctggacta 20

<210> 37
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> primer ECa5'-1600

<400> 37
caccaataaa tgcagagact tc 22

<210> 38
<211> 26
<212> DNA
<213> artificial sequence

<220>
<223> primer 3125

<400> 38
aatccatcat ttctcattac agtgtg 26

<210> 39
<211> 879
<212> DNA
<213> *Ehrlichia canis*

<220>
<223> nucleic acid sequence of *E. canis p28-1*

<400> 39
atgaataata aactcaaatt tactataata aacacagtat tagtatgctt 50
attgtcatta cctaatatat cttcctcaaa ggccataaac aataacgcta 100
aaaagtacta cggattatat atcagtggac aatataaacc cagtgtttct 150
gttttcagta atttttcagt taaagaaacc aatgtcataa ctaaaaacct 200
tatagcttta aaaaaagatg ttgactctat tgaaaccaag actgatgcca 250
gtgtaggtat tagtaaccca tcaaatttta ctatccccta tacagctgta 300
tttcaagata attctgtcaa tttcaatgga actattggtt acacctttgc 350
tgaaggtaca agagttgaaa tagaaggttc ttatgaggaa tttgatgtta 400
aaaaccctgg aggctataca ctaagtgatg cctatcgcta ttttgcatta 450
gcacgtgaaa tgaaaggtaa tagttttaca cctaaagaaa aagtttctaa 500
tagtattttt cacactgtaa tgagaaatga tggattatct ataatatctg 550
ttatagtaaa tgtttgctac gatttctctt tgaacaattt gtcaatatcg 600
ccttacatat gtggaggagc aggggtagat gctatagaat tcttcgatgt 650
attacacatt aagtttgcat atcaaagcaa gctaggtatt gcttattctc 700
taccatctaa cattagtctc tttgctagtt tatattacca taaagtaatg 750
ggcaatcaat ttaaaaattt aaatgtccaa catgttgctg aacttgcaag 800
tatacctaaa attacatccg cagttgctac acttaatatt ggttattttg 850
gaggtgaaat tggtgcaaga ttgacattt 879

<210> 40
<211> 293
<212> PRT
<213> *Ehrlichia canis*

<220>

<223> amino acid sequence of *E. canis* p28-1 protein

<400> 40

Met Asn Asn Lys Leu Lys Phe Thr Ile Ile Asn Thr Val Leu Val
5 10 15

Cys Leu Leu Ser Leu Pro Asn Ile Ser Ser Ser Lys Ala Ile Asn
20 25 30

Asn Asn Ala Lys Lys Tyr Tyr Gly Leu Tyr Ile Ser Gly Gln Tyr
35 40 45

Lys Pro Ser Val Ser Val Phe Ser Asn Phe Ser Val Lys Glu Thr
50 55 60

Asn Val Ile Thr Lys Asn Leu Ile Ala Leu Lys Lys Asp Val Asp
65 70 75

Ser Ile Glu Thr Lys Thr Asp Ala Ser Val Gly Ile Ser Asn Pro
80 85 90

Ser Asn Phe Thr Ile Pro Tyr Thr Ala Val Phe Gln Asp Asn Ser
95 100 105

Val Asn Phe Asn Gly Thr Ile Gly Tyr Thr Phe Ala Glu Gly Thr
110 115 120

Arg Val Glu Ile Glu Gly Ser Tyr Glu Glu Phe Asp Val Lys Asn
125 130 135

Pro Gly Gly Tyr Thr Leu Ser Asp Ala Tyr Arg Tyr Phe Ala Leu
140 145 150

Ala Arg Glu Met Lys Gly Asn Ser Phe Thr Pro Lys Glu Lys Val
155 160 165

Ser Asn Ser Ile Phe His Thr Val Met Arg Asn Asp Gly Leu Ser
170 175 180

Ile Ile Ser Val Ile Val Asn Val Cys Tyr Asp Phe Ser Leu Asn
185 190 195

Asn Leu Ser Ile Ser Pro Tyr Ile Cys Gly Gly Ala Gly Val Asp
200 205 210

Ala Ile Glu Phe Phe Asp Val Leu His Ile Lys Phe Ala Tyr Gln
215 220 225

Ser Lys Leu Gly Ile Ala Tyr Ser Leu Pro Ser Asn Ile Ser Leu
230 235 240

Phe Ala Ser Leu Tyr Tyr His Lys Val Met Gly Asn Gln Phe Lys
245 250 255
Asn Leu Asn Val Gln His Val Ala Glu Leu Ala Ser Ile Pro Lys
260 265 270
Ile Thr Ser Ala Val Ala Thr Leu Asn Ile Gly Tyr Phe Gly Gly
275 280 285
Glu Ile Gly Ala Arg Leu Thr Phe
290 293

<210> 41
<211> 840
<212> DNA
<213> *Ehrlichia canis*

<220>
<223> nucleic acid sequence of *E. canis p28-2*

<400> 41
atgaattata agaaaattct agtaagaagc gcgttaatct cattaatgtc 50
aatcttacca tatcagtctt ttgcagatcc tgtaggttca agaactaatg 100
ataacaaaga aggcttctac attagtgcaa agtacaatcc aagtatatca 150
cactttagaa aattctctgc tgaagaaact cctattaatg gaacaaattc 200
tctcactaaa aaagttttcg gactaaagaa agatggtgat ataacaaaaa 250
aagacgattt tacaagagta gctccaggca ttgattttca aaataactta 300
atatcaggat tttcaggaag tattggttac tctatggacg gaccaagaat 350
agaacttgaa gctgcatatc aacaatttaa tccaaaaaac accgataaca 400
atgatactga taatggtgaa tactataaac attttgcatt atctcgtaaa 450
gatgcaatgg aagatcagca atatgtagta cttaaaaatg acggcataac 500
ttttatgtca ttgatggtta atacttgcta tgacattaca gctgaaggag 550
tatctttcgt accatatgca tgtgcaggta taggagcaga tcttatcact 600
atttttaaag acctcaatct aaaatttgct taccaaggaa aaataggtat 650
tagttaccct atcacaccag aagtctctgc atttattggt ggatactacc 700
atggcgttat tggtaataaa tttgagaaga tacctgtaat aactcctgta 750
gtattaaatg atgctcctca aaccacatct gcttcagtaa ctcttgacgt 800
tggatacttt ggcggagaaa ttggaatgag gttcaccttc 840

<210> 42

<211> 280

<212> PRT

<213> *Ehrlichia canis*

<220>

<223> amino acid sequence of *E. canis* p28-2 protein

<400> 42

Met Asn Tyr Lys Lys Ile Leu Val Arg Ser Ala Leu Ile Ser Leu
5 10 15

Met Ser Ile Leu Pro Tyr Gln Ser Phe Ala Asp Pro Val Gly Ser
20 25 30

Arg Thr Asn Asp Asn Lys Glu Gly Phe Tyr Ile Ser Ala Lys Tyr
35 40 45

Asn Pro Ser Ile Ser His Phe Arg Lys Phe Ser Ala Glu Glu Thr
50 55 60

Pro Ile Asn Gly Thr Asn Ser Leu Thr Lys Lys Val Phe Gly Leu
65 70 75

Lys Lys Asp Gly Asp Ile Thr Lys Lys Asp Asp Phe Thr Arg Val
80 85 90

Ala Pro Gly Ile Asp Phe Gln Asn Asn Leu Ile Ser Gly Phe Ser
95 100 105

Gly Ser Ile Gly Tyr Ser Met Asp Gly Pro Arg Ile Glu Leu Glu
110 115 120

Ala Ala Tyr Gln Gln Phe Asn Pro Lys Asn Thr Asp Asn Asn Asp
125 130 135

Thr Asp Asn Gly Glu Tyr Tyr Lys His Phe Ala Leu Ser Arg Lys
140 145 150

Asp Ala Met Glu Asp Gln Gln Tyr Val Val Leu Lys Asn Asp Gly
155 160 165

Ile Thr Phe Met Ser Leu Met Val Asn Thr Cys Tyr Asp Ile Thr
170 175 180

Ala Glu Gly Val Ser Phe Val Pro Tyr Ala Cys Ala Gly Ile Gly
185 190 195

Ala Asp Leu Ile Thr Ile Phe Lys Asp Leu Asn Leu Lys Phe Ala
200 205 210
Tyr Gln Gly Lys Ile Gly Ile Ser Tyr Pro Ile Thr Pro Glu Val
215 220 225
Ser Ala Phe Ile Gly Gly Tyr Tyr His Gly Val Ile Gly Asn Lys
230 235 240
Phe Glu Lys Ile Pro Val Ile Thr Pro Val Val Leu Asn Asp Ala
245 250 255
Pro Gln Thr Thr Ser Ala Ser Val Thr Leu Asp Val Gly Tyr Phe
260 265 270
Gly Gly Glu Ile Gly Met Arg Phe Thr Phe
275 280

<210> 43
<211> 828
<212> DNA
<213> *Ehrlichia canis*

<220>
<223> nucleic acid sequence of *E. canis p28-3*

<400> 43
atgaactgta aaaaaattct tataacaact acattggtat cactaacaat 50
tcttttacct ggcatatctt tctccaaacc aatacatgaa aacaatacta 100
caggaaactt ttacattatt ggaaaatatg taccaagtat ttcacatttt 150
gggaactttt cagctaaaga agaaaaaaac acaacaactg gaatttttgg 200
attaaaagaa tcatggactg gtggtatcat ccttgataaa gaacatgcag 250
cttttaatat cccaaattat tcatttaaat atgaaaataa tccatttta 300
ggatttgcag gggtaattgg ctattcaata ggtagtccaa gaatagaatt 350
tgaagtatca tacgagacat tcgatgtaca aaatccagga gataagttta 400
acaatgatgc acataagtat tgtgctttat ccaatgattc cagtaaaaca 450
atgaaaagtg gtaaattcgt ttttctcaaa aatgaaggat taagtgacat 500
atcactcatg ttaaatgtat gttatgatat aataaacaaa agaatgcctt 550
tttcacctta catatgtgca ggcattggta ctgacttaat attcatgttt 600
gacgctataa accataaagc tgcttatcaa ggaaaattag gttttaatta 650

tccaataagc ccagaagcta acatttctat gggtgtgcac tttcacaaag 700
taacaaacaa cgagtttaga gttcctgttc tattaactgc tggaggactc 750
gctccagata atctatttgc aatagtaaag ttgagtatat gtcattttgg 800
gttagaattt gggtacaggg tcagtttt 828

<210> 44
<211> 276
<212> PRT
<213> *Ehrlichia canis*

<220>
<223> amino acid sequence of *E. canis* p28-3 protein

<400> 44

Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Thr Leu Val Ser Leu
5 10 15
Thr Ile Leu Leu Pro Gly Ile Ser Phe Ser Lys Pro Ile His Glu
20 25 30
Asn Asn Thr Thr Gly Asn Phe Tyr Ile Ile Gly Lys Tyr Val Pro
35 40 45
Ser Ile Ser His Phe Gly Asn Phe Ser Ala Lys Glu Glu Lys Asn
50 55 60
Thr Thr Thr Gly Ile Phe Gly Leu Lys Glu Ser Trp Thr Gly Gly
65 70 75
Ile Ile Leu Asp Lys Glu His Ala Ala Phe Asn Ile Pro Asn Tyr
80 85 90
Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Val
95 100 105
Ile Gly Tyr Ser Ile Gly Ser Pro Arg Ile Glu Phe Glu Val Ser
110 115 120
Tyr Glu Thr Phe Asp Val Gln Asn Pro Gly Asp Lys Phe Asn Asn
125 130 135
Asp Ala His Lys Tyr Cys Ala Leu Ser Asn Asp Ser Ser Lys Thr
140 145 150

Met Lys Ser Gly Lys Phe Val Phe Leu Lys Asn Glu Gly Leu Ser
155 160 165
Asp Ile Ser Leu Met Leu Asn Val Cys Tyr Asp Ile Ile Asn Lys
170 175 180
Arg Met Pro Phe Ser Pro Tyr Ile Cys Ala Gly Ile Gly Thr Asp
185 190 195
Leu Ile Phe Met Phe Asp Ala Ile Asn His Lys Ala Ala Tyr Gln
200 205 210
Gly Lys Leu Gly Phe Asn Tyr Pro Ile Ser Pro Glu Ala Asn Ile
215 220 225
Ser Met Gly Val His Phe His Lys Val Thr Asn Asn Glu Phe Arg
230 235 240
Val Pro Val Leu Leu Thr Ala Gly Gly Leu Ala Pro Asp Asn Leu
245 250 255
Phe Ala Ile Val Lys Leu Ser Ile Cys His Phe Gly Leu Glu Phe
260 265 270
Gly Tyr Arg Val Ser Phe
275

<210> 45
<211> 813
<212> DNA
<213> *Ehrlichia canis*

<220>
<223> nucleic acid sequence of *E. canis p28-9*

<400> 45
atgaattaca aaagatttgt tgtaggtgtt acgctgagta catttgtttt 50
tttcttatct gatggtgctt tttctgatgc aaatttttct gaagggagga 100
gaggacttta tataggtagt cagtataaag ttggtattcc caattttagt 150
aatttttcag ctgaagaaac aattcctggt attacaaaaa agatttttgc 200
gttaggtctt gataagtctg agataaatac tcacagcaat tttacacgat 250
catatgaccc tacttatgca agcagttttg cagggtttag tggtatcatt 300
ggatattatg ttaatgactt tagggtagaa tttgaaggtt cttatgagaa 350

ttttgaacct gaaagacaat ggtaccctga gaatagccaa agctacaaat 400
tttttgcttt gtctcgaaat gctacaaata gtgataataa gtttatagta 450
ctagagaata acggcgttgt tgacaagtct cttaatgtaa atgtttgtta 500
tgatattgct agtggtagta ttcctttagc accttatatg tgtgctggtg 550
ttggtgcaga ttatataaag tttttaggta tatcattgcc taagttttct 600
tatcaagtta agtttggtgt caactaccct ctaaatgtta atactatgtt 650
gtttggtggg ggttattacc ataaggttgt aggtgatagg catgagagag 700
tagaaatagc ttaccatcct actgcattat ctgacgttcc tagaactact 750
tcagcttctg ctactttaaa tactgattat tttggttggg agattggatt 800
tagatttgcg cta 813

<210> 46
<211> 271
<212> PRT
<213> *Ehrlichia canis*

<220>
<223> amino acid sequence of *E. canis* p28-9 protein

<400> 46
Met Asn Tyr Lys Arg Phe Val Val Gly Val Thr Leu Ser Thr Phe
5 10 15
Val Phe Phe Leu Ser Asp Gly Ala Phe Ser Asp Ala Asn Phe Ser
20 25 30
Glu Gly Arg Arg Gly Leu Tyr Ile Gly Ser Gln Tyr Lys Val Gly
35 40 45
Ile Pro Asn Phe Ser Asn Phe Ser Ala Glu Glu Thr Ile Pro Gly
50 55 60
Ile Thr Lys Lys Ile Phe Ala Leu Gly Leu Asp Lys Ser Glu Ile
65 70 75
Asn Thr His Ser Asn Phe Thr Arg Ser Tyr Asp Pro Thr Tyr Ala
80 85 90
Ser Ser Phe Ala Gly Phe Ser Gly Ile Ile Gly Tyr Tyr Val Asn
95 100 105

Asp Phe Arg Val Glu Phe Glu Gly Ser Tyr Glu Asn Phe Glu Pro
110 115 120
Glu Arg Gln Trp Tyr Pro Glu Asn Ser Gln Ser Tyr Lys Phe Phe
125 130 135
Ala Leu Ser Arg Asn Ala Thr Asn Ser Asp Asn Lys Phe Ile Val
140 145 150
Leu Glu Asn Asn Gly Val Val Asp Lys Ser Leu Asn Val Asn Val
155 160 165
Cys Tyr Asp Ile Ala Ser Gly Ser Ile Pro Leu Ala Pro Tyr Met
170 175 180
Cys Ala Gly Val Gly Ala Asp Tyr Ile Lys Phe Leu Gly Ile Ser
185 190 195
Leu Pro Lys Phe Ser Tyr Gln Val Lys Phe Gly Val Asn Tyr Pro
200 205 210
Leu Asn Val Asn Thr Met Leu Phe Gly Gly Gly Tyr Tyr His Lys
215 220 225
Val Val Gly Asp Arg His Glu Arg Val Glu Ile Ala Tyr His Pro
230 235 240
Thr Ala Leu Ser Asp Val Pro Arg Thr Thr Ser Ala Ser Ala Thr
245 250 255
Leu Asn Thr Asp Tyr Phe Gly Trp Glu Ile Gly Phe Arg Phe Ala
260 265 270
Leu
271